

Copyright (c) 1993 - 2005 Compugen Ltd.							
OM protein - protein search, using sw model							
Run on:	February 16, 2005, 16:16:11 ; Search time 38.2706 Seconds (without alignments)						
Title:	US-10-003-356-8						
Perfect score:	4904						
Sequence:	1 MPERRKEQDEGPGIHEFLAR.....TVSTVLDLDRVLIMCPLXIQ 927						
Scoring table:	BLOSUM62						
Searched:	283416 seqs, 96216763 residues						
Total number of hits satisfying chosen parameters:	283416						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing: Minimum Match 0%							
	Maximum Match 100%						
Database :	PIR_79:*						
	1: PIR1:*						
	2: p12:*						
	3: pr3:*						
	4: pir4:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
	SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description		
1	1695.5	34.6	1085	2 S40476	Ca(2+)-sensing receptor		
2	1690.5	34.5	1079	2 I59362	calcium/polyvalent calcium receptor		
3	1687.5	34.4	1078	2 A56715	calcium receptor		
4	1673.5	34.1	1088	2 B56715	taste receptor TR		
5	845	17.2	858	2 JC7683	metabotropic glutamate receptor		
6	835.5	17.0	879	2 JC7160	glutamate receptor		
7	821.5	16.8	1218	2 S71376	metabotropic glutamate receptor		
8	814.5	16.6	879	2 JH0562	metabotropic glutamate receptor		
9	795.5	16.2	1180	2 JC2132	metabotropic glutamate receptor		
10	795.5	16.2	1212	2 JC2131	metabotropic glutamate receptor		
11	794	16.2	1199	2 A41939	G protein-coupled receptor		
12	776	15.8	1171	2 A42916	metabotropic glutamate receptor		
13	764	15.6	872	2 JH0561	metabotropic glutamate receptor		
14	758	15.5	915	2 A49874	metabotropic glutamate receptor		
15	724.5	14.8	871	2 A46742	metabotropic glutamate receptor		
16	707.5	14.4	912	2 JH0563	metabotropic glutamate receptor		
17	691.5	14.1	1267	2 T2131	metabotropic glutamate receptor		
18	679	13.8	908	2 I49142	metabotropic glutamate receptor		
19	656	13.4	999	2 T27628	metabotropic glutamate receptor		
20	398	8.1	551	2 T30806	metabotropic glutamate receptor		
21	296	6.0	1099	2 T16283	metabotropic glutamate receptor		
22	215	4.4	921	2 T51136	metabotropic glutamate receptor		
23	211	4.3	923	2 F84732	metabotropic glutamate receptor		
24	194	4.0	997	2 S33754	metabotropic glutamate receptor		
25	188	3.8	933	2 C96495	metabotropic glutamate receptor		
26	186.5	3.8	1039	2 T45779	probable ligand-gated glutamate receptor		
27	168.5	3.4	953	2 E84732	probable ligand-gated glutamate receptor		
28	163	3.3	960	2 JE0356	gamma-aminobutyric acid receptor		
29	157	3.2	950	2 T51134	ionotropic glutamate receptor		
	RESULTS						
	RESULT 1						
	S40476						
	Ca(2+)-sensing receptor - bovine						
	C;Species: Bos primigenius taurus (cattle)						
	C;Date: 19-Mar-1997 #sequence_change 09-Jul-2004						
	C;Accession: S40476						
	R.Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; I: Nature 366, 575-580, 1993						
	A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from mouse mammary gland						
	A;Reference number: S40476; PMID: 8255296						
	A;Accession: S40476						
	A;Status: preliminary						
	A;Molecule type: mRNA						
	A;Residues: 1-1085 <BRO>						
	A;Cross-references: UNIPROT: P35384; NID: 9453108; PIDN: AAB29171.1; PID: 945310.						
	Query Match 34.6%; Score 1695.5; DB 2; Length 1085;						
	Best Local Similarity 39.3%; Pred. No. 3.8-116; Mismatches 323; Indels 45; Gaps 15;						
	Matches 350; Conservative 173; MisMatches 323; Indels 45; Gaps 15;						
	Query 53 LVIGGLPPIPDSTTPITKSYSTEAVLYPLTGQB--ENRPNTNSTGAFPA--GIVGAGGSPLSV 166						
	Db 33 IIIGGLPFIHFGVAVKDQLSKSRPESVCIRYNRGRFWLQAMIPATEINSSPALLPNM 92						
	Query 112 TIGXQIPTCFITKSYSKPLTQFPLTGQB--ENRPNTNSTGAFPA--GIVGAGGSPLSV 166						
	Db 93 TIGYRIPDTCNFVSKAELATLSPVAAQNIDSLSLDEGCNCSEHPSTIAVVGATGSGSII 152						
	Query 167 PASRLGHYYLLPOQVGTISTCVLSDKYQPPSYLIRVIASDKTOSKAVVKRIQHGGWVNGA 226						
	Db 153 AVNLGLFYIPOVSYASSRSLSNQKFSPLTITINDEHQATAMADIEYFRWNNGT 212						
	Query 227 IADDGYKGYVTKERKMEASNLCAVAFSETIPKVKSYNEKAVKVTSTAKVIVLYT 286						
	Db 213 IADDGYGPGEKFEREEBRDICIDSELISIQSYSDEBKIQVVEVQNSPAKVVVFS 272						
	Query 287 SDIDLSIYVLENTHNTDTDTATBWIITSALAKPBYFPPYFGTTGFATPSVTPOLK 346						
	Db 273 SGDLBPLIKEITVRNNTGRWIASEAASSLJAMPBYFHVGTTGFGLKAGQIPGFR 332						
	Query 347 EPLYDVHBNPKDNDVLTIBFWQTAFNCTWPNSSSVPNVDHRVNMTGKEDRLYDMSDQ- 403						
	Db 333 EPTQKVHPRKSYHNQFAKEFWETFNCHLOEGAKGPLPVDF-TFLRGHEEGGARLNSPT 390						
	Query 404 ---LCGGBEKLQDRLKTYLDTQSLRITKQCOVAYIAHGDHLSPCQBGOPFGSNQQ 459						
	Db 391 AFRPLCTGBENISSVERPYMDTHLRSYNTVLAIVSIAHALQDITYTCIPGRGLP-TNGS 449						
	Query 460 CAYIPTPEWQWLMYKYMCEIKPFSHEDKWLJLDNGDILKJNGHYDVLMLWHLD-DEGEIETFTV 518						
	Db 450 CADIKKVEAWQVLKHLRHLNFTSNMGQVTPDCGDLA-GNYSINWHLSPDGSIVFKB 508						

Result 3	
519 VGRFNFASTNFFLVIPINSTFWNTESRDRPHSCTDVCPPGTRGFVOREPICFDSIP	578
509 VGYINTYAKKGRFLPDKLWGSRSREFFSNSRDLAATKGLIGEPTCFCPEVY	568
579 CADGHVRSKPGERECECGDQEWNSAQKSECVLKEVEYLAYDEALGFTAVILSYGAFYV	638
569 CPGEYSDETADASACDKPDPDEWSNENHTSSIAKEAEFLSWTEPPGIALTFLAVLGIFLT	628
639 LAVTAVVYIHRHTPLYNASDWOLGELIQVLSIIMIULSSMFLIDKPHNWSCMAGQVTLAIG	698
629 AFLGVTPKFRTPITVKATNRBLSYUFLSFSLCCFSSLLPFTGEQDWTRRLRPAFGIS	688
699 FSLCLSCULGTSSLFLAYRISKSKTQLTSHPLTRK-----IVLVLISVLARIGIC	750
689 FVLCISCLVKTNRVLLVF--BAKLP-TSH-----RKWWGJNLQFLVFLCTFMQIVICA	741
751 AYJLEPPMVYKMESESONTKTTLGCNEISIBFLYSMNGFIDFLALICFLUTFVARQLPDN	810
742 IWINATAPSSYRNHBLDEBIFITCHGSSLMALGFLIGTYLLAACPFPAFKSRKLPEP	801
811 YYEGKCIITFGMLVFFIWMSPYVVLSTKGKPKMAVEIPAIALLASHGLUCIFAPKCLII	870
802 FNEAKFTFSMLIFFIVWISFTPAYASTYTGKPSAVEVIAITLAASFLACIFFNKVYII	861
871 LLAPERNTSEIVGGRVSTTDNCIQLTSAFV-----SSELINNTTVST 911	
862 LFKPSRNTIEV-RCSSTAHHFKVAARATLRRSNVSQRSSSLGGSTGST 910	
Result 2	
599 624 acidium/polycyclic cation-sensing receptor precursor - rat	
Species: Rattus norvegicus (Norway rat)	
Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004	
Accession: AAC52195.1; PID:97905	
DB: Ratt. M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.	
DB: Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995	
Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals	
Reference number: 159362; MUID:9521465; PMID:7724534	
Accession: 159362	
Molecule type: mRNA	
Residues: 1-1079 <RES>	
Cross-references: UNIPROT:P48442; EMBL:U20289; NID:9790578; PID:97905	
Experimental source: striatal	
Experimental source: Ricciardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.	
Experimental source: National Acad. Sci. U.S.A. 92, 131-135, 1995	
Title: Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor	
Reference number: AAC52195.1; MUID:9521465; PMID:7816802	
Accession: AAC52195.1	
Molecule type: mRNA	
Residues: 1-133, 'X', 135-1079 <RIC>	
Cross-references: GB:U10354	
Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein	
Experimental source: kidney	
Domain: transmembrane #status predicted <SIG>	
:1-20/Domain: signal sequence #status predicted <SIG>	
:187-212/Region: hydrophobic	
:613-635/Domain: transmembrane #status predicted <TM2>	
:650-670/Domain: transmembrane #status predicted <TM3>	
:683-700/Domain: transmembrane #status predicted <TM3>	
:725-744/Domain: transmembrane #status predicted <TM4>	
:770-790/Domain: transmembrane #status predicted <TM5>	
:806-828/Domain: transmembrane #status predicted <TM6>	
:841-860/Domain: transmembrane #status predicted <TM7>	
:90, 261, 287, 386, 488, 594, 893, 1005/Binding site: carbohydrate (Asn) (covalent) #status predicted <SIG>	
:794/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted <SIG>	
:899, 901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted <SIG>	
Score: 1690.5; DB 2; Length 1079;	
Best Local Similarity: 38.0%; Pred. No. 8.7e-116;	
Matches 352; Conservative 18%; Mismatches 332; Indels 61; Gaps 17;	
11 LALLWHSAYGPDRAQKGSD	54
75 PASAKCEGENFORFWMKAMIMHKIKNKKDILPNITLGQIFDTCTSKSVEAVLVL	134
55 PESVCRTRNFRGFLWQAMIAFEIIBINSPESSLPMNTLGRIFDTCTVSKALEATLSP	114
135 LTQBD--ENRPNPENSTGAPPA-GIVGAGGSFLSPVAPASRILGLYLYLPQVGYTSTCIVL	189
75 PASAKCEGENFORFWMKAMIMHKIKNKKDILPNITLGQIFDTCTSKSVEAVLVL	134
115 VAQNKRIDSUNLDEFNCNSEHIPSTIAVGATGSGYSTAVANLGLGLPTIPQSYASSRRL	174
190 SDKYOPPSYRVIASDKIQSKAVVRIQHPRGWWVGAIAADDYKGKVTKPEKMESEN	249
175 SNKNQYKSPRTIPDEHQATAMADIEFPRWNWTGTAADDYGRGEGIEKREEAERD	234
250 LCVAFSETIPKVSNEMKOMAKAVKVTSTAKVIVLYTSDIDL-SLFVLEMIHENITDDTWI	309
235 ICIDSELISYSDEREIQQVEVENTSTAKVIVVESGPDPLELIKIVRNNTGIRWL	294
310 ATEAATISALIAKPSYFYPRFGTGTATPRSVIPGKLEFIDYDHPNPKDNDVLTIEPOT	369
295 ASEAWASSSSLJAMPEFYHVVGGTGFGLKACQIPGFBFLQKVHPRSVHNGPAKEFWB	354
370 AFNC7WPNS---VPVNVDHRVNMTCGEDRLYDMSD---OLCTGEGBLLEDLKNTYLDTSQ	423
355 TPNCHLQEGAKGKPLPVDTFVRSHEEG-GNRLNNSPAPRPLCTGDENTINSVTPYMPYEH	413
424 LRITKOCKQAYATAIAHGLDHLSRCQSGQPFPSNOOQAYIPTPDFWQMLYMKIEIKFKSH	483
414 LRISTNVYLVASIAHLQDIYTCFLPORGFL-TNGSCADIKKVEAWYQKLRLHNFTNN	472
484 EDKWWVILLDDNDLKNKHYDVNLWHLD-DEGETSFVTVGRGNFRSTNFPLVIPNTNSTIFVN	542
473 MGEQVTFDECDLV-GRYSTINWHLSSEDGSIVPKETGYINTYAKKGRFLIMEKEILW	531
543 TESSRLPHSVCTDVCPPGTCRGFVQBPICCPDSIPCAQDGHVSRKPGERECEOHDYMS	602
532 GFSRETFNSNSRDCQNGTRKQIIGEPTCCEBCVEPDGEVSGETDASACDQPDPDFWS	591
603 NAQKSECVLKEYEYLADEAQLGFTLVLISVFGAFVULAVTAVVHHTPLVNASDWQLG	662
592 NENHTSIAKEBEFLAWTEPFGTAIATPLAVGIFTAVLGFPIKFRNTPIVKATNREL	651
663 FHIQVSHIIMJLSSMLFDKPHNWSNAGQVTLALGFLSCLCLGRTSSLFLAYRISKS	722
652 YLLFLPSLICCFSSSLPFIGEPODWTCILRQAFGISMVFCISCLVTKNTRVLLVPE-	-EA 708
723 KTLQLTSHPHPLYK-----LIVLISVLAETIGCTAYTILEPMMVYKMEQSNTKIIILG	774
709 K1P-TSPH--EKKWGNLNOFLFLVFLTEPFGTAIATPLAVGIFTAVLGFPIKFRNTPI	764
775 CNEISIEPLYSMGIDAFIALLCFLITFVQRLPDNTYEGKCTIFGMLYFFIIMMSFV	834
765 CHGSLMAGLGSUJGTYCTLLAALCFFFAFKSRKLPENFNEAKFTFMSLIFWTFIPA	824
835 YLSTKGKPFKMAVEIFATLASSHOLLGCIAPKCLLILRPERNTSEIVCGRVSTTDNCIQ	894
835 YASTYGFPSVAVTIAAASFGULACIFPENKVYILFKPSRNTIEV-RSSTAAHAFK	882
895 LTSAFV-----SSLENNTVVS 910	
893 VAARATIRRPNTSRKRSSLGSGTS 908	
Calcium receptor (clone phPCaR-4.0) - human	
Ci:Species: Homo sapiens (man)	
Ci:Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text_change 01-Dec-2000	
Ci:Accession: A56715 #sequence revision 149419; C9419	
R; Garrett, J.B.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; He	
J. Biol. Chem., 270, 12919-12925, 1995	
A title: Molecular cloning and functional expression of human parathyroid calcin	

A;Reference number: A56715; MUID:95279439; PMID:7759551
A;Accession: A56715
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: GR:1-1078 <GR>
A;Residues: 1-1078
A;Cross-references: GR:U20759; NID:9683744; PIDN:AAA86503.1; PID:9683745
A;Pearce, S.H.S.; Thakker, R.V.
Submitted to the EMBL Data Library, August 1994
A;Reference number: S9341
A;Accession: S9341
A;Molecule type: DNA
A;Residues: 1-180 'Q' 182-989 'R' 991-1078 <PEA>
A;Cross-references: EMBL:X81086
A;Reference number: A9419; MUID:94094324; PMID:791660
A;Accession: A9419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 178-192 <POL>
A;Experimental source: Family N
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 186Arg mutation is associated with familial hypocalciuric hypercalcemia and nec
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
A;Accession: B4919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 289-303 <PO2>
A;Experimental source: family E
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 298lys mutation is associated with familial hypocalciuric hypercalcemia and nec
A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
A;Accession: C4919
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 788-802 <PO3>
A;Experimental source: family J
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 796trp mutation is associated with familial hypocalciuric hypercalcemia and nec
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match Score 1687.5; DB 2; Length 1078;
Best Local Similarity 38.0%; Pred. No. 1.5e-115;
Matches 353; Conservative 179; Mismatches 333; Indels 63; Gaps 18;

Db 18 LAPLW-AELGSAKEKEEERTCRLLGKCVDAENHSLVIGLPPIDSRTIPANESI-LB 74
Db 19 LALTWHTSAYGPQRQAQKGD-----IILGGLPFPFHGVAKDQDLKSR 54
Db 75 PASAKCCEGFNFQPRFMKAMIMIKENKRKDILPNTLGQIFDTCTFISKSVEAVLF 134
Db 55 PESVETCYRFNRGFRNLQAMIAPIEINISSPALLPNLGRFIDCNTVSKALEATLSF 114
Db 135 LTCQB---ENRPNFRNSTGAFPA-GIVTAGGSSFLSTYASRFLGTYLPGTYTSTCIVL 189
Db 115 VAGNKIDSNLNDFCNCSEBHPISTIAVGATSGVSTAVANLGLFTPQSYASSRRL 174
Db 190 SDKYQPPSPYLRTIASDKLQSCKAVVKRQHQFGKWWGAIAADDYDGKYGKTCFKERNESAN 249
Db 175 SNQNQPKFLRTLPNDEHQATAMADILYFRNWVGTLAADDYDGREGIEKFREAFERD 234
Db 250 LCVAPSETIPKVSNERKQKAVKTKSTAKVTKVLYTSIDISLFLVIMHNITDWTI 309
Db 235 ICIDRSELISQYSDEELQHVYEVIONSTAKVIVVFFSGPDLEPLIKEVRNITGKWL 294
Db 310 ATREWITSLIAKPEPYTFGGTTGFAFPTSYTGLEFLYDHPNQDPNDVLTIFWQT 369
Db 295 ASEAWASSSLIAMQYFHVGGTIGALQJPGFRFLKKVHPRSVHNGFAKFWEB 354
Db

Qy 370 APNC-TWPNSSUPVYDHRVNMTGKE--DRLYMDSD--OLCTGEKLEDLKNTYLDTS 422
Db 355 TENCHLQEGAKCPLEVDF--TEURGHESGDFDSNSSTAERPLCTGDENISSEVTPTDYT 412
Qy 423 QRTTRCKOQAVYTAIAGLDHLSRCORGQGPFSNOOCAYZPTFDWQLMTYMKBTKFKS 482
Db 413 HLRISSTNVVLAIVSIAHALDIYTCLPGRGLP-TNGSCADIKKVEAWQVLKHLRHNFNT 471
Qy 483 HEDKWTLLDDNGDLKNGKHYDVLNWHD-DEGBISFTVYGRFNRSTNFBLVTPNSTFW 541
Db 472 NNGBQVTFDDECDCLV-GNYSLINWWHUSPEDSIVFGRGVYNNVYAKGBRLPINBKLW 530
Qy 501 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 531 SGCSREVPSNSRCDLCAIGTRGKITEBPTCPFCVCPDBSYSDTDASACNKCOPDFW 601
Qy 542 NTBESRPLPHSVUTDVPPTGRGPWQRBPICCFDSIPCADCAGHSRKPGERCEOCGBDW 601
Db 591 SNENTTSCTIAEIEPLSWTPEFGIALTFLAVGFLTAFLVGFVKFRNTTIVKATNREL 650
Qy 602 SNAQKSECVLKEVYVLADEALGFTLVILSYGFATVLAIVAVYVTHRTPLVNAWDQWL 661
Db 651 SYLLFLSLLCCFSSSLFPIGEQPDWTCRLRPAFISPVLCISCLVKTNRVLLVE--E 707
Qy 662 GFLQVSLIMLMSMLPFLIDKPHNNSCMAGOTVLLAUGFSLCLSLIGHTKTSLLFLAYRISK 721
Db 722 SKTQTSMHPLYRK-----IVLISLVLABIGCTAYLLEPPMVYKOMESONTKILL 773
Db 708 AKIP-TSFH--RKWGLNLQFLPFLCMTMQIVCIVWLYTAPPSSYRNQNBLEDITIFI 763
Qy 774 GCNEISITEFLYNSMFGIDAFLALLCFLTTFLVVARQDNPNEYGKCTITGMLVPPFIWMSFV 833
Db 764 TCHEGSMLAFLGIFTCLLAAICPFPAFKSRKLPPENENBAKFPITSMLIFIVWNSFIP 823
Qy 834 VYLTSGKGFKNAAVEFPAIASSHGLGCIAPKCLLILLREBERTSBIVCRVSTTDNCI 893
Db 824 AYASTYGFVSAAVEVAILAASFGLACIPFKNVIYILPKFSRNTTIEV--RCSTAAHAF 881
Qy 894 QLTSAFY-----SSRLANNTVST 911
Db 882 KVAARATLRRSERNSRKRSSSUGGSTST 909

RESULT 4
B56715 calcium receptor (clone phPCar-5.2) - human
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C;Accession: B56715
R;Garrett, J.B.; Capuano, I.V.; Hung, B.M.; Hebert, S.
J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecule cloning and functional expression of human parathyroid calcium receptor
A;Reference number: A56715; MUID:9279439; PMID:7759551
A;Accession: B56715
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: GB:U20760; NID:9683746; PID:9683747
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match Score 1673.5; DB 2; Length 1088;
Best Local Similarity 37.6%; Pred. No. 1.6e-114;
Matches 353; Conservative 180; Mismatches 332; Indels 73; Gaps 19;

Qy 18 LAFLW--AEIJSBARBERKEBERTCRLLGKCVDAENHSLVIGLPPIDSRTIPANESI-LB 74
Db 11 LALTWHTSAYGPQRQAQKGD-----IILGGLPFPFHGVAKDQDLKSR 54
Qy 75 PASAKCCEGFNFQPRFMKAMIMIKENKRKDILPNTLGQIFDTCTFISKSVEAVLF 134
Db 55 PESVETCYRFNRGFRNLQAMIAPIEINISSPALLPNLGRFIDCNTVSKALEATLSF 114
Qy 135 LTCQB---ENRPNFRNSTGAFPA-GIVTAGGSSFLSTYASRFLGTYLPGTYTSTCIVL 189
Db 115 VAGNKIDSNLNDFCNCSEBHPISTIAVGATSGVSTAVANLGLFTPQSYASSRRL 174
Qy 190 SDKYQPPSPYLRTIASDKLQSCKAVVKRQHQFGKWWGAIAADDYDGKYGKTCFKERNESAN 249
Db 175 SNQNQPKFLRTLPNDEHQATAMADILYFRNWVGTLAADDYDGREGIEKFREAFERD 234
Db 250 LCVAPSETIPKVSNERKQKAVKTKSTAKVTKVLYTSIDISLFLVIMHNITDWTI 309
Db 235 ICIDRSELISQYSDEELQHVYEVIONSTAKVIVVFFSGPDLEPLIKEVRNITGKWL 294
Db 310 ATREWITSLIAKPEPYTFGGTTGFAFPTSYTGLEFLYDHPNQDPNDVLTIFWQT 369
Db 295 ASEAWASSSLIAMQYFHVGGTIGALQJPGFRFLKKVHPRSVHNGFAKFWEB 354
Db

QY	190	SDKYQFPSPYLRTIASDKIQSKAVVRIQHGTWVGAIAADDYQKYGKTFKEKMESEN	249	C;Superfamily: metabotropic glutamate receptor 4
Db	175	SNKNQPFSSFLRTIPNDHEQTAAMADIEFWNNWGTIAADDGPGSKPREEAERD	234	C;Keywords: transmembrane protein
QY	250	LCVAFSETIPKVYSNERKMRQAKAVAKVARTSTAKIVLYTSDIDLSEFLMENIHNNITDRTWI	309	Query Match Score 17.2%; Length 858;
Db	235	ICIDFSELISQTSDEBIIHQHVEETONSTAKIVYVFSSGPDLEPLIKEVRRNNTGKWL	294	Best Local Similarity 28.0%; Pred. No. 8.8e-54;
QY	310	APEAWITISALIAPKPEVPPYFGTTGATPATPSVIGLKEPLYDVEPNKDNDVLTIEPTQ	369	Matches 238; Conservative 164; Mismatches 382; Indels 66; Gaps 23;
Db	295	ASERAWASSSLAMPQTFFHVVGGTGPALKAGQIPDFREFKKYHPRKSWSNGFAKEFWE	354	QY 54 VIGGLPFDSDRTIPANESILEPASAEGENPQRPRMKAMIKMKEINRKRDILPNINTL 113
QY	370	APNC-TWPNSSPVYNTDHRNMTCR---QLCTGEELKEDLNKNTLPDS	422	Db 36 TLLGGFLPFGSSTERATLNRTPNTSIPCNTRFSPLGLFLAMAMKNAVEELINGSALLPGRL 95
Db	355	TNCHLQEGAKGPLPTD---TPLRGHEESGRFSNSSTARPLCIGDENISSVTPYIDT	412	QY 114 GYQIPDTCPTISKSVEAVLVFLTG-QEENRPNFRNSTAASP---AGIVEAGGSFSIUSPASR 170
QY	423	QLRITKOCKQAVAYIAHGLDHLSRCOEGGQPFGSNQOCAYIPTDFEWQMLMMYKKEIKPKS	482	Db 96 GYDLDFTICSEPVTVMKSSLMELAKVGOSOSIAACNTQYOPRVLAVIGHPSSELAIRGK 155
Db	413	HLRISTINVAYLAVSYIAHALQDIYTCLPGRLF-TNGSCADIKCYEAOWKLHLRHNNTN	471	QY 171 IUGLYLQFQGVGYTSTCYTSLDKYQFSYSLRVIASDKIOSKAVYKRIQHFGWVWVGAIAAD 230
QY	483	HEDKWKIILDDGDLKNGHVDLNWHLD-DGEIGSFVTVGRENFRSTINPELVIPTNSTIFW	541	Db 156 PFSFPLMPQVSYSASMDRLSDRETFPSIFRTVPSDRVOLQAVTTLQNSWNVAALGSD 215
Db	472	NNGEQVTFDECGLDV-GNYSSTINHNLSPNSGIVSVEKEYVQYNYAKCGERLFINEEKILW	530	QY 231 DDYKGKCVGKTFKEMESANLYCAFSESTIPIKVSN---EKMQKAVKAVKTSTAKIVLYT 286
QY	542	NTESS-----RLPHSVCTDVCPPTGTRGTVQREPICCPDSIIPADGHYSRKPGER	591	Db 216 DDIIDLSLSPVLEMHNHTDRTWIAWITSALLIAKEBYFPYFGGTGATPESVIPGLK 346
Db	531	SGFSSREPLTFVLSVQVPFNSCSRULCAAGTRKG1IEGETFCCFECVCEPGEYSDETDAS	590	QY 287 SDIDLSLSPVLEMHNHTDRTWIAWITSALLIAKEBYFPYFGGTGATPESVIPGLK 346
QY	592	EBCBQCGEDYWNNAQSKBCVLRKEVEYTLAYDEALGFTLVILSVSVEAFVUFLATAVAYVTHRH	651	Db 276 SARAVYSLFSYSSIHGSISKWVVAASWLTSDLVMTLPNIARYGTVLGFLQNGALLP--- 332
Db	591	ACNKCPCDPDFNSNENHNTSCLAKEIETLSWTEPFGITALTEAVLGFILTFAVLGFLVFIKRNT	650	QY 347 EPLYDWPN---KDPNDVLTIBFWQDPAFNCTWPNSSPYVNDVHRVNTGKBDRLYD-M 400
QY	652	PVNNSDWQGLFQVLSLIMLSSMLFDKPHNWSCMAGQVTLALGFSLCSCLIGHTS	711	Db 333 EFSHYETHLALAADP-----AF-C-----ASLNALEDLIEHVMGQRCPRCDDIM 376
Db	651	PIVKATNREUSYLFLSLLCPSSSSLFLFGEQDQWTCRQPAFGISPLCSCILVKTN	710	QY 401 SPOLCTGBEKLEDLNKTYLDTSQLRITKOCKAOVAYIAHGLDHSRCLGQGQPFGSNQQC 460
QY	712	SIFLAVRISRSKTKTQLTSMPLYRK-----IVLISLVLAEIGCTAYLLEPPMYK	763	Db 377 LQNLSGG---LIQNLSCAQOLH_HQ1PIT---YAAYVSYQAQALINTLQCNVSHCIVSEH--- 427
Db	711	RVLLVP---EAKIP-TSFH---RKMWGLNQFLVLFCTFMQVIVCIVWVLTAPPSSYRN	763	QY 461 AYIPTDFWOLMYYMKEIKPKFSHEDKWKVILDNDGDLKNGHVDLNNTWLDDEGEISFTYVG 520
QY	764	MESONTKTIIGCNE-SIEFLYMSMGIDATALLLFLTYVARQDNYEGKCOITFEMLV	823	Db 428 -VLP---WQLENMNMMSFHA-RDQTLQFDAEGNV-DMEYDLMWVQSPPTPV-LRTVG 479
Db	764	QELEDSTIFTCHESLMAFLGFLIGYCTLAAICPPFKRSKLPENENAKPITSMLI	823	QY 578 PCADGIVSVREGEREBCQCGDYSWNAQSKBCLKEVLEYLAYDEALGFTLVLSVGRAFV 637
QY	824	FIIWISFVPPYFLSTPKKFKAWEVIAFIAIASHSRLGCTFAPCLLITLRRPNTTSIVC	883	Db 528 DCKAGGSYRKHDPPDTCTPCNODQWSSEKSTACLPRPKFLWGEPPVVLILLCLVIGL 587
Db	824	FIIWISFVPPAYASTYGFVSAEVIAIASHSRLGCTFAPCLLITLRRPNTTSIVC	882	QY 638 VLAVTAVYVTHRHTPLYNASDWQGLFLQIVOSLIMLSSMLFLIDKPHNWSCMAGQVTLAL 697
QY	884	GRVSTDIDNCIQLTSAFV-----SEBLANNTVST	911	Db 588 ALAALGLSVHEWDSPVQASGSGSQQFCGLICLGLFLCISVLLPGPGRSSASCLAQQPM AHL 647
Db	883	-RCSTAAHAFKVAARATLIRSNSVSRKRSISLGSSTGST	919	QY 698 GFSLCISCLGLKTSSIFLAVR-ISSKSTQLTSMHFLYRKLTIVLISVIAEIGCTAYLIL 755
QY	756	BPPMVTKNMESQNTKILGNEISIEFLYMSMGIDATALLLFLTYVARQDNYEGK	815	Db 648 PLTGCTISTLFLQAAELFVSEHPLSVAWNLCSYLRLSWLAVLTFVEAALCAWYLIA 707
QY	708	GPPEVTDWSVLPTEVLEHCHVRWSVSLGLVHITNMMLAFLCPLGFLVQSOGRNTRAR	767	RESULT 5
Db	816	CITFGNLVFFFIMMSPVTPVLTSTKGRKFMATEIFAIALLSHGLGCCIFAPKCLLILRPE	875	JC7683 taste receptor T1R3 - mouse
QY	768	GUTFAMLAYFPTWVSBVPLIANVQVYQPAVQMGAIIVLCALGILVTFHLPKCYVLLMLPK	827	C;Species: Mus musculus (house mouse)
Db	876	RNTSEIVCGR 885	Db;Accession: JC7683	
Db	828	LNTQEFFLGR 837	C;Comment: This protein, a seven-transmembrane receptor subtype 3 precursor - mouse	
			C;Species: Mus musculus (house mouse)	
			C;Genetics:	
			A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste.	
			A;Reference number: JC7683; MUID:21222794; PMID:11322794	
			A;Contents: tongue	
			A;Molecule type: mRNA	
			A;Residues: 1-858 <KIT>	
			C;Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994	
			C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the sig	
			C;Accession: JC7683	
			C;Genetics:	
			A;Gene: tlr3	
			A;IMAP position: 4	

RESULT 6
JC7160 metabotropic glutamate receptor subtype 3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Genetics:
C;Accession: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

Accession: JC7160	635	KPSPVTCALRRLGLTSFAICYSLCLTNTNCLARIATGQKPKTPSSQQVFCIG 694
:Minoshima, T.; Nakanishi, S.	636	
:Biochem. 126, 889-896, 1999	637	
:Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3	638	
:1-24/Domain: signal sequence #status predicted <SIG>	639	
:25-879/Domain: transmembrane glutamate receptor subtype 3 #status predicted <TM1>	640	
:577-599/Domain: transmembrane #status predicted <TM2>	641	
:614-634/Domain: transmembrane #status predicted <TM2>	642	
:646-664/Domain: transmembrane #status predicted <TM3>	643	
:689-709/Domain: transmembrane #status predicted <TM4>	644	
:735-756/Domain: transmembrane #status predicted <TM5>	645	
:770-791/Domain: transmembrane #status predicted <TM6>	646	
:804-828/Domain: transmembrane #status predicted <TM7>	647	
Query Match Score 17.1%; Best Local Similarity 26.8%; Matches 242; Conservative 167; Mismatches 389; Indels 105; Gaps 31;	648	Length 879;
Score 835.5%; DB 2; Pred. No. 4.5e-33; C:Accession: S71376	649	#text_change 09-Jul-2004
Keywords: differential regulation; G protein-coupled receptor; receptor; transmembrane protein	650	C:Sequence _revision 17-Apr-1998
1-24/Domain: signal sequence #status predicted <SIG>	651	R; Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
:25-879/Domain: transmembrane glutamate receptor subtype 3 #status predicted <TM1>	652	FEBS Lett. 392, 71-76, 1996
:577-599/Domain: transmembrane #status predicted <TM2>	653	A; Title: Cloning and characterization of a bifunctional metabotropic receptor a
:614-634/Domain: transmembrane #status predicted <TM2>	654	A; Reference number: S71376
:646-664/Domain: transmembrane #status predicted <TM3>	655	A; Accession: S71376
:689-709/Domain: transmembrane #status predicted <TM4>	656	A; Status: not compared with conceptual translation
:735-756/Domain: transmembrane #status predicted <TM5>	657	A; Molecule type: mRNA
:770-791/Domain: transmembrane #status predicted <TM6>	658	A; Residues: 1-1218 <KUB>
:804-828/Domain: transmembrane #status predicted <TM7>	659	A; Cross-references: UNIPROT:O90ZP3
RESULTS 7	660	C; Keywords: Glycoprotein; phosphoprotein
S71376	661	F:603-625/Domain: transmembrane #status predicted <TM1>
lvgggfpidsrtipanesislepasakcegfnqr-frmwkmamimkbeinkrdilpn 111	662	F:640-660/Domain: transmembrane #status predicted <TM2>
lvlgglfpinergktgtpee-----crginedrgiqrlqamlfaideinkndvllpgv 89	663	F:672-690/Domain: transmembrane #status predicted <TM3>
112 tlgcyqfdptc---ptisksveavnlvtflgoenprnfrnstgap-----agivg 158	664	F:717-737/Domain: transmembrane #status predicted <TM4>
90 klgvhildtcsrdtysaleqlslefvrasltslydb--aeymcpdgsyaiqnepnpli 147	665	F:761-782/Domain: transmembrane #status predicted <TM5>
159 agggspfsvpsarpsilgltpqgytstpcvtilsdykqckavvriion 218	666	F:796-817/Domain: transmembrane #status predicted <TM6>
148 gsyssvsiqvaniqlrlfqipqisyastsaksdsksrydyfartrvpdpdyqakamabilr 207	667	F:826-850/Domain: transmembrane #status predicted <TM7>
219 fgwwygaladddygkrygktrtkermesaniicvaafsetipkvysmekmokavk-avkts 277	668	F:104-233, 403, 525, 757/Binding site: carbohydrate (Asn) (covalent) #status predi
208 fnwtystvsargdygetgtieafeqarlnrciataekvrsnirksydsivtrelljkp 267	669	F:636, 699, 961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
278 takvilytstdidlsleflvleminthnitdrtwiateawitsaliak-peffpyfggtigfa 336	670	F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi
268 narvvlfmrssdsreliaasrvn-asfttwyasdmgqaobsivkgsehway-gratls 324	671	F:892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predi
337 tprsvifgkleyflvdypnkdopndvlteifotafnctwissvptvndvrrvnmtckdr 396	672	Query Match Score 16.8%; Best Local Similarity 25.6%; Matches 228; Length 1218;
325 lashpvrqfdptfqslmpynhrnpwfdrfslqmkqr-----nhr----- 370	673	Conservative 182; Mismatches 372; Indels 109; Gaps 29;
397 lydmsdolctgeekledkntyltdtsqrliitkqckrovaytaahgldhlsr - coeqqgp 454	674	Score 821.5%; DB 2; Pred. No. 7.6e-52;
371 -----qic-dkhlaidsnyeqeskimfv---vnaavyahahikmqrliucp----- 413	675	Missmatches 372; Pred. No. 7.6e-52;
455 gsnqqcayiayiptdfwqmy-ymkbeirk-----ksbedkwylldngdlknghydtlnw- 506	676	Indels 109; Gaps 29;
414 nttklcdamkldgkkydkylkintatapfnpkngadsvtukfdtg-d-gmgrinyvnfq 472	677	
507 hlddegsisfttvgrfmfrstnfelvlpntstifwntessrlphsvctdwpptgrgvf 566	678	
473 hig---grkysiykgwh-----aetylvdvdsihwrns-----vptsoqdcpapnenkn-m 521	679	
567 orepiccfds1pcadghvskrp-----gerceqcdgywmaqsekcvkevlayds 621	680	
522 qgdvuccwicpc-----epyeylvdefcmcdcgfgoqptadsgccylnpedyrwed 574	681	
622 algfthvltlsvgafyvlatavaayvihtrplvlnasdwolqfliqvslimllsmlf1d 681	682	
575 awaigpvtiacylqfmcmtcivtqkmtplvkaqrelcylvllfgvsvcmppffia 634	683	
682 kphnwscmagsqytalqfslcslcglktssulfatrisksktolts-mphlyrkivl 740	684	
323 raildtkvkrktstarkvilyttsdidslfylemmihunit-drtwiateamttsaliak 223	685	
265 -ekmqkavkavktstarkvilyttsdidslfylemmihunit-drtwiateamttsaliak 322	686	
280 fdlrlkreb-rlpkaravvcfcgmpvsiplvqkmlrrgqagepllgsgwdaddevb 338	687	
323 psypfyggttigfatiptsvipulqkelydvhphnkopndvltiefwvotaefncmwnpsvyp 382	688	

Db	339	GYEQAEGG-ITVKLKHSEEVTSFDDYFLKLRLNTNTRNPWFPEWQHRCRIPGHPE-	396	Qy	53	LVIGGFFPIDSRTIPANESILEPASAKCEGENFOR FRWKAMIAIMIKEINIKRDKDILPNI 111
Qy	383	NVDHKYNTMGKEDRLYDMSDQLC7GEEKEKDLENLYTDLTSQURITKROCKQNTAYAHLGD 442		Db	39	IVLGGFRPINKEKGTCPE----- -CGRNEDIGIQRLAEMLPIDEKNDVYLPGV 89
Db	397	NMNYKRN-----CSGYESEL-----CSGYESEL-----CSGYESEL-----CSGYESEL-----		Qy	112	TLGXOFLDTC---FTISKSEVAINTFLTOBENRNRNSTGAFP-----AGIVG 158
Qy	443	-HLSRCQEGQPFGSNOQCAYIPTDFWQLMYMKELKFK--SHEDKWLIDDDNGDNLKN 498		Db	90	KLGVHLDTCERDTYALEQSLEFRAISLTYDE-AEYMPDGSYAIQENIPLLAGVIG 147
Db	436	DMHSHCOP-----OHVGCKAMPIDSGQLEFLMITSFTGSGEDW--FDENGDTP- 486		Qy	159	AGGSFSPVASRULGLYJLPGVGTSTCVLSDKYQFPSYLVRIASDKIOSKAVVRIOH 218
Qy	499	GHYDVLNWHDGEGRISFTVGRPNFRSNTNFELVPIPTNSTFWNTTESSRLPHSVCTDVCP 558		Db	148	GSYSSVTVQANLLRFQIPOLYSTATSACLSDKSYYDFTARTVPPDFYQAKAMABLRF 207
Db	487	GRYEMLNQVTPGAFDYNVGSWHEGQNSID-----DYMQINNSDMVLSVCSPCS 539		Qy	219	FGWWWTGAIADDYDCKYGVKTEKEKMESENLCVARSSETIPKVYSNEKMQAVK - AVKTS 277
Qy	559	PGTGROFQVOREPICAFDS1PCADQHVSXPKGERECEQCCEDYMSNAQKSECVLKEYEYL 618		Db	208	FNWTVYTVSTVSEGDQSEGTLTAAFEQBARLRNCTIATAEKGVRSNIRSYDSVTRELIQKQP 267
Db	540	KGEIKVTRKGEVSCWCWICACKONEIVQ--DEFICTACADLGWPDPPELEGEPITRLYE 597		Qy	278	TAKVTVLYTSDIDLISFVLEMHIHNTDRTWIAATEWITSALIAK PEYFPYFGGTGFA 336
Qy	619	YDEALGFTPLVILSVEGAFLVLTAVAVYTHRTPLVNASDWQFLTQLQSLTMLLSSMML 678		Db	268	NARVTVLFMRSSD-SRELIAANRVNQJASFTWASDVGWAQESIVKGSSEHVAY-GALTLE 324
Db	598	WGNPESIVQYVQACAGLIVLTSFETVFLYVYDTPVVKSSRECYLILGIGYICPFT 657		Qy	337	TPRSVTPGLKBRFLYDTHPNKDPDNVLTIEFWQTAFNCTWPNSVSPYDHRYNMTGKEDR 396
Qy	679	FIDKPHNWSMAGQVTLAAGLFSCLSLQKTTSSLKQTSKTSRSMHPLY----- 733		Db	325	LASHPVQRFDRYFQSTINPYNNHNPFRDFWEQKFQCSLONKR--NHR----- 370
Db	658	LIAQPTVASCYLQRLLNGSATMCYSLVTKTNE--IARLLASSKKKCTRKPREMSAWA 715		Qy	397	LYDMSDQLCTGEEKLLEDLKNTYLTDSOLRITKQCKQDAVAYAHLGDLHLSR --COEGQGP 454
Qy	734	RKIVLVLSTLAEGIICATVLLIREPMMYKOMMSEONTKILGCGNEISIEFLYSMEGIDAFL 793		Db	371	-----OYC--DGHLLADSSNQEKRIMFV--VNAVYAHALHMORTLCP----- 413
Db	716	OLVIAGLIVSVOLTLEVTLTLEPPMVPVSYSPSR-EVFLCINTSTVG--MVAPLGNGL 773		Qy	455	GSNQQCAVYIPTPDFWQI-MYTMKEIKP-----KSHEDKWKVILDQNDLKNKHYDVLNW 507
Qy	794	ALLCFLTTFVARQLPDNYVYSGKCTIFGMLYFFLWIMSPYVYIYSTKGFKRMAYEFAILLA 853		Db	414	NTTKLQCDAMKLLDKGKLUKEYVLLKINNTAEPNPNKQGADSIVKTFDTFCD-GMGRYVNFNLQ 472
Db	774	IMSCTYAFAKTRNVANERAKYTAFTMNTCTIILAFPIYFGS--NYKLTTSFSEVYL 831		Qy	508	LDDGEISFVTVGFRFRSTNFELVPTNSTLFWNTESSRLPHSCTVDPVCPGTRGTVQ 567
Qy	854	SSHGLIGCIFAPKCLLILRPERN-----TSLIV-----CRVSTTDNCI 893		Db	473	QTGGKTSYLVKHW-----AETLSDLDVDSIHWNSNS - VPTSQSDPCANEMKNN-MQ 522
Db	832	SYTVALGCMFSPSKVITYLAKERFVNRSFTSDVRRMVGDGTVNACRSNSL 882		Qy	568	REPICCFDSTIPICADGHVSRKP-----GERECQGEDIYWSNAQKSECVLKEYLAYDBA 622
Db	523	PSDVCWCICP-----EPBYLWDEFTCMDGPQWPATDSLGCYCNLPEDYTKWEDA 575		Db	623	LGFTLVLISVPAFVYLAVTAVYVHIRTPLYNASDQKGLFJLQVSJLIMLSSMLFDK 682
Qy	JH0562	metabotropic glutamate receptor 3 precursor - rat		Qy	576	WAIGPTTIAQGLFLCTIVITYFKKNTPLTKASGRELYCYTFLGVSLSYCMTPFLAK 635
C	Species: Rattus norvegicus (Norway rat)		Db	683	PANWSMCAGQVTLAAGSLSLCSCLGKTTSFLAYRISKSXTQTS-MHPLXRYKIVLIS 741	
C	Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004		Qy	742	VLABIGCICAYTILEPPMV--YKMNQESONTKILGCBNISIPLYSMFGIDAFALLCPL 799	
C	Accession: JH0562		Db	696	ILVQINVNVSVWILLETGTRRYTLPERRET-VILKCNVYKDSSMLISL-TYDVLVILCTV 753	
C	Comment: This protein is coupled to a G protein and evokes a variety of functions by n		Qy	800	TTFVAROLPDNYEGKCTITFGMLUVFETIIMSFPVPUVLTSGKPKMATEFIAIASHG- 857	
C	Superfamily: metabotropic glutamate receptor 4		Db	754	YAFKTRICPENFNEAKTGFMYTTCIWIWALFLPIFTSSDVRQITTMCSYLSGFV 813	
C	Keywords: G protein-coupled receptor; Glycoprotein; phosphoprotein; transmembrane protein		Qy	858	LIGCIFARKCLLILRPERNTSEIVGRVSTTDNCIQLTSAFVSELMNTTVSTLDDRV 917	
P	1-22/Domain: signal sequence #status predicted <SIG>		Db	814	VLGCLPAKVKVHTLFQPOQN--VVTHRHLNRFSVSATTYSQSSASTYVPTCNGRE 870	
P	577-599/Domain: metabotropic glutamate receptor 3 #status predicted <TRI>		Qy	918	LI 919	
P	614-634/Domain: transmembrane #status predicted <TRI>		Db	871	VL 872	
P	689-709/Domain: transmembrane #status predicted <TRI>				RESULT 9	
A	Residues: 1-879 <TRAN>				metabotropic Glutamate receptor 5 A - human	
A	Cross-references: UNIPROT:P31422				C Species: Homo sapiens (man)	
A	Experimental source: brain				C Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996	
C	Comment: This protein is coupled to a G protein and evokes a variety of functions by n				C Accession: JC2132	
C	Superfamily: metabotropic glutamate receptor 4				R;Minakami, R.; Katsumi, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.	
C	Keywords: G protein-coupled receptor; Glycoprotein; phosphoprotein; transmembrane protein				Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994	
P	735-756/Domain: transmembrane #status predicted <TRV>					
P	757-759/Domain: metabotropic glutamate receptor 3 #status predicted <TRI>					
P	804-828/Domain: transmembrane #status predicted <VII>					
P	829-842/439/Binding site: carbohydrate (Asn) (covalent) #status predicted					
P	861-884/Binding site: phosphate (Ser) (covalent) #status predicted					
P	610,845/Binding site: phosphate (Ser) (covalent) #status predicted					

A;Title: Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor 7						
A;Accession: JC2131; MUID:94197696; PMID:7908315						
A;Molecule type: mRNA						
A;Residues: 1-1180 <MIN>						
C;Comment: This protein is coupled to guanine nucleotide binding proteins.						
C;Keywords: G-protein; neurotransmitter; receptor; transmembrane protein.						
F;Domain: 580-640;Domain: transmembrane #status predicted <TM1>						
F;617-637;Domain: transmembrane #status predicted <TM2>						
F;644-664;Domain: transmembrane #status predicted <TM3>						
F;694-714;Domain: transmembrane #status predicted <TM4>						
F;739-759;Domain: transmembrane #status predicted <TM5>						
F;773-794;Domain: transmembrane #status predicted <TM6>						
F;803-827;Domain: transmembrane #status predicted <TM7>						
Query	Match	Score	795.5;	DB 2;	Length	1180;
Best	Local Similarity	25.6%	Pred. No.	6e-50;		
Matches	224;	Conservative	180;	Mismatches	359;	Gaps
					113;	29;
Qy	53	LVIIGGLFPIDSRTIPANESILEPPASAKC---EGFFNFORFRMMKAMITMHMKEINKRKDIL	108			
Db	35	IIIGALFSVHHQ--PTVDKTHE--RKCGAVRBDIGIQH--YEAQMUTLBRINSDPFL	86			
Qy	109	PNITLGQIIPDTCP---TISKSIAVNLVPLTGEEENRNP---NSTGAAFP-----GT	156			
Db	87	PNITLGCETRDSCHNSAVALEQSTEFIORDLSISSEEEGLVRVCYDGSSSSPRKKPPIVGV	146			
Qy	157	VGAGSFLSPVSPASRLGGLYLPQCVYQTSTCIVLDKYQPPSYVIRVIASDKIQSRAVYKRI	216			
Db	147	IGPGSSSSVAQVNQLQLQFLPQKAYSATSMDSLKDILKLYKVKVVPSPDAQQARAWDIV	206			
Qy	217	QHFQMYWVGATAADDGYKGKVTKFKEKNESANLCAVAPSETIPKVVSNEMOKAKRAVKT	276			
Db	207	KRYNTTYVSAVHTBEGYSGMEAKPDMSAKEGICIAHY--KIVYSNAGEQSFDKLKK	263			
Qy	277	ST---AKTIVLWTSDISLFLVEMIHNIIT-DRTWIAATEW----ITSALLARPKY	325			
Db	264	LTSHLPKARVVAFCACGTMVTRGLIMAMMRGLAGAEFLIJGSDGMADRYDVTDG-----	316			
Qy	326	PPYFGGTIGPATPRTSVIPGJK---BFLDVYHPNPKDNDVLTIEWTOAFTNCN---WPNSS	379			
Db	317	--QYRERAVGGTTKICQSPDVKWFLDYLKLRPPTTHRNWFQEWTQHFRQCLEGFPOPEN	374			
Qy	380	VPYNYDHRVNMTGKDRDLYDMSDQLCCTGEEKLRLIKNTLDTTSOLRITKQCRQAYAVALA	439			
Db	375	SKRNKTCNSSSL-----LKHThVQDSMGMFV---INAIVSMDAY	409			
Qy	440	GIDH--LSCRCOEGQPFQFGNGQCAQYIPTDFQWLMYMKRBIKPKSHEDDKWILDNGDLK	497			
Db	410	GLHNHQMSLCP-----GTAAGLCDAKKPLDGKRLLESMLKTNFTGVSGDTILPDEENGDS	462			
Qy	498	NGHDYDVLNWHDDEGEISPTVGRGNFRSTNFBVLIPTNSTIFNTESRLPHSVCTDVC	557			
Db	463	PGRYEIMPKEMKGKQFYDINNGSD---NGEKAAMDDEV--W-SKSKSNITRSVCSRPC	515			
Qy	558	PPGTGRGFVQREPICCFCDSP1PCADGHVSRKPGGERCEQGEDWNSAQKSECVLKKEYYL	617			
Db	516	EKGQKTVKIRKGEBVCCWTPCKNEYVF--DETICKACOLGSPTDDLGCDLIPVYOL	573			
Qy	618	AYDBALGFTVILSFGAFVFLAVATVYVTHRPLUNASDWQJGLFLOVSLIMLSSM	677			
Db	574	RWGDPPEPIAVVFAFCIGLIALTFVFLYRDPVVKSSRELCYILLAGICUGYLGCTF	633			
Qy	678	LPIIDKPHNWSMAGQVTLAUGFSLCLSLGKTSSSLFLAYRISKSKTQTSMPHFLY---	733			
Db	634	CLIAFKQITCYLQRIGIGPSANVSYALSALVTRKTR--IARILAGSKKLCTRKPRFISAC	691			
Qy	734	-RKIVLIVSILVLAEGIICATVLLRPPMVYKMBSONTKILGCBMBSIEFLYSMFGIDAF	792			
Db	692	AQLVIAFLCILQIOLGIVALFIMPBDIMEDYPSR-EYVILCHNTTNGL-WVTFGLNG	749			
Qy	793	IALLCPLFTTFVARQELDPNTEGKCTFGMUVFIIWMSVTPVISTKGKRNAAVEIF	852			

Qy 618 YDEALGFFTLVLSVFGAVFLAVTAVVTHRTPLYNASDWOLGFLLQVSLLIMISSLW 677
 Db 574 RWGDPPIAIVVAFGLIATLFTVVFLYRDPVVKSSRLCYTILAGICLGYLCTP 633
 Qy 678 LFIDKPHNNSCMAGVTALGFSCLSLCKDSSLFAYRISKSKTQLTSMPHLY---- 733
 Db 634 CЛИАРКРQTCYLCRIGLGSAMPSYSALTAKTR--TARILAGSKKCTKTPREMSAC 691
 Qy 734 -RKIVLVLISLAEGICLAYLIEPPMVTKNMQSNTQKTLGENEISIEFLYSMFGIDAP 792
 Db 692 AQLVIAFLCILQGILTVALFIMPDDHYSIR-EVYLICNTTNG-VUTPLGYNGL 749
 Qy 793 LALLCPLTIVVARQLPDNYYEGKCTIFGNLVFFFILMNSFVPLSTKGKFMVAEFLAI 852
 Db 750 LILSCPTFYAKTRNPNANFEAKTYAFTMNTTCIWLAFVPIFGS--NYKIIITMCFSV 807
 Qy 853 ASSHGLLGCFIAPKCLLILRPERN-----TSEIV 882
 Db 808 LSATVALGCMFVKYVIIILAKPERNVRSAFTSTVV 843
 Qy 825 CTTTTFYARQLPDNYYEGKCTIFGMVVFELIWMSPFVYPLSTKGKFMVAEFLASH 856
 Db 825 VALGCMFPTPKMYIIILAKPERNVRTSDVV 856

RESULT 11

A41939 G protein-coupled glutamate receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A41939; S15362
 R;Homaled, K.M.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, Science 252, 1318-1321, 1991.
 A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate receptor
 A;Reference number: A41939; MUID:92022526; PMID:165624
 A;Accession: A41939
 A;Status: Preliminary; not compared with conceptual translation
 A;Residues: 1-1199 <HOU>
 A;Cross-references: UNIPROT:P23385; GB:M61099; NID:9397806; PID:AAA19497.1; PMID:9204460
 A;Experimental source: cerebellum
 A;Source: sequence extracted from NCBI backbone (NCBIP:60785)
 R;Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.
 A;Title: Sequence and expression of a metabotropic glutamate receptor.
 A;Reference number: S15362; MUID:91156047; PMID:1847995
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1199 <HMA>
 A;Cross-references: EMBL:X57569; NID:956646; PID:CAA40799.1; PID:956647
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match Score 794; DB 2; Length 119;
 Best Local Similarity 26.0%; Pred. No. 7.9e-50;
 Matches 27; Conservative 179; Mismatches 364; Indels 102; Gaps 31;

Qy 53 LVIGGLFPIDSRTPANESTILEPASAKC---EGFNFORFRMKAMTHMIKEINKRDL 108
 Db 45 VIGAFLSVHHQ--PPAEKVY--RKGCHIREOGIQI--VFLTGQENRPNRNSTGAPP----- 153
 Qy 97 PNITLGSEIRDSCHMSSVVALEQSLEFIRDLSLISRDEKGLNRCLPDCGTLPPGRTKKP 156
 Qy 154 AGIVGAGGSFLUSVPAASRLGHYLPQVGTTSTCVLSDYQFPEYLRYTASDKIQSKAVV 213
 Db 157 AGVIGPQSSVVAIQVNQLQFDIQAISATSIDLSDTLYKFLRVPSDTLQARAML 216
 Qy 109 PNITLGQIIFDTCP---TISKSVEAV--LVFLTGQENRPNRNSTGAPP----- 153
 Db 177 PNITLGSEIRDSCHMSSVVALEQSLEFIRDLSLISRDEKGLNRCLPDCGTLPPGRTKKP 156
 Qy 214 KRIQHFGWWYQGIAADDYDGKYGKTFKEKMEANLYCASETIPIKYSN-----EKM 267
 Db 217 D1VKRNTWYTSVAVHTEGNGESGDAFELAQAEGLCAHSD---KIVSNAGEKSFDRL 273
 Qy 268 QKAVKAVKTSTAKVIVLTYSTDIDLSLFLVLEMHNIN-TDRTWIAEANTSAJAKPEYF 326
 Db 274 LRLKLRS-RLPKARVVCFCBEGMTVRGLSAMRLLQGVGGFSLIGSGDWADEVIEGYEV 332

RESULT 12

A42916 metabotropic glutamate receptor mGluR5 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A42916
 R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
 A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 co-
 A;Reference number: A42916; MUID:92317054; PMID:13200017
 A;Accession: A42916
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1171 <BB>
 A;Cross-references: UNIPROT:P31424; GB:D10891; NID:9220813; PID:BA01711.1; PID:d100218
 A;Experimental source: brain
 A;Note: sequence extracted from NCBI backbone (NCBIP:107749; NCBIP:107750)
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match Score 776; DB 2; Length 1171;
 Best Local Similarity 24.9%; Pred. No. 1.6e-48;
 Matches 218; Conservative 185; Mismatches 361; Indels 110; Gaps 29;

Qy 53 LVIGGLFPIDSRTPANESTILEPASAKC---EGFNFORFRMKAMTHMIKEINKRDL 108
 Db 35 IIIGALFSVHHQ--PTVDKVHE--RKGCHIREOGIQI--VFLTGQENRPNRNSTGAPP----- 153
 Qy 109 PNITLGQIIFDTCP---TISKSVEAV--LVFLTGQENRPNRNSTGAPP----- 153
 Db 177 PNITLGSEIRDSCHMSSVVALEQSLEFIRDLSLISRDEKGLNRCLPDCGTLPPGRTKKP 156
 Qy 214 KRIQHFGWWYQGIAADDYDGKYGKTFKEKMEANLYCASETIPIKYSN-----EKM 267
 Db 217 D1VKRNTWYTSVAVHTEGNGESGDAFELAQAEGLCAHSD---KIVSNAGEKSFDRL 273
 Qy 268 QKAVKAVKTSTAKVIVLTYSTDIDLSLFLVLEMHNIN-TDRTWIAEANTSAJAKPEYF 326
 Db 274 LRLKLRS-RLPKARVVCFCBEGMTVRGLSAMRLLQGVGGFSLIGSGDWADEVIEGYEV 332

QY 158 GAGGSEFLSYVAPASRILIGLYLIPQVGTYTSTCIVLSDKQYQQPSYLRYIASDKIOSKAVVKKRIQ 217
 Db 147 GPQSSSVAAQVNULQLPNQPIAYSASTMDSBDKTLKRYFQKVWPSAQQARAMYDVK 206
 QY 218 HEGWNVGAIADDGYGVTKPKEKMEANLICVAPSETIPIKVSN--EIQMKAVKAV 274
 Db 207 RYNTTYVAVHTEGNNGSGMEEAKDMASAKEGICIAHSY--KIVSNPGEQSFDKLUKTL 263
 P; 203, 286, 338, 402, 547/Binding site: carbohydrate (Asn) (covalent) #status predicted
 QY 275 KT--STAVKIVLTVLTDIUSLFLVLEMHNIT-DRTWIAEAN----ITSALLIAKPEYF 326
 Db 264 RSHLPKARVVACFCEGMTRGILMAMRRLGLAGEPLLGSLGDAWRDVTDTG---- 315
 QY 327 PYFGCTIGIFATPSPV1PKGLK--EFLYDVFHNPKDPNDLTIEFWQTAFNCTWNENSSVYN 383
 Db 316 -YQRBAAVGIGITIKUQSPDVYDYLKLQRPTNLRNWQFOBZQHREOC----- 364
 QY 384 VDHFRVNMTCGKEDRILYD--MSDQLCTGBCLEKEDLKNTYLDTSQRLRITKOCKQAVVYIAHGL 441
 Db 365 ---RLEGFAQENSCKNCNTCNSSLTLLRTHVQDSRMGFV-----INAISYMAGL 410
 QY 442 DH--LSCR0EGQGPFGSNOQCAV1PTPFDWQLMYMRKIEFKSHEDKWLDDNGDURG 499
 Db 411 HNMQMSLCP-----GYAGLCDAKMPIDCRKLDSLMTNTNFTGVSQDMILPDENGD SPG 463
 QY 500 HYDYLNWHDGEGRISFVTVGRENFRSTNFELVTPNTNSTIWFNTESRSLPHSYCTDYPCC 559
 Db 464 RYBIMNFKEMKGKDYFDYINGSDW---NGELKMDDDV--W-SKNNNIRSVCSBPEK 516
 QY 550 GTGRGQVREPICCFDS1PCADGHVSRKGPERCEQCGEDYNSNAQKSECVLKEVEVYAY 619
 Db 517 GQIKVTRKSEVSCCWTCPCKENEVYVF--DEYTKACCOLGSNSPTDDLGCDLJIPVQYLRW 574
 QY 620 DEALGFTLVLSVFGAFVFLATAVVYIHRHTPLVNAWDWQLQFLIVSLIMLSSMLF 679
 Db 575 GDPEPIATAVVFACIGLILATLFLTVPIYRDTPVVKSSRELTYILLAGICUGLYCTFCI 634
 QY 680 IDKPHNWNSCMAGOTVLALGFSLCLSLCILGKTSSLFLAYTRISKSTKTOLSMHPY---R 734
 Db 635 IAKPKQIYXCYLQLRGIGJGSPMSVSYALVTRKTNR--IAAILAGERKKK1CTKPRFMSAACQ 692
 QY 735 KIVLIVSLAEIGCTAYLILEPPMVYKOMESONTKILLGCNEBISIEFLYSMFGIDAFLA 794
 Db 693 LVIAPFLICLIOGLTIVALFIMEPDMDYPSIR-EVYLICHTTNLG-VVTPIGYNGLI 750
 QY 795 LLCLPLTTFYARQLDNYTEGKCTPFGMUVFFIWMSTPFPVYUStSTKGRKMAVEIFALAS 854
 Db 751 LSTCFYAFKTRNVPANFNEYKAFTMYYTCIWLAFPIYFGS--NYKIIITMCFSVSL 808
 QY 855 SHGLGCTIPAKCILJILLRPERN----TSEIV 882
 Db 809 ATVALGMMFVPKVYIILAKPERNTRSAFTSTVV 842
 RESULT 13
 JH0561 metabotropic glutamate receptor 2 precursor - rat
 C Species: Rattus norvegicus (Norway rat)
 C Accession: JH0561
 R; Tanabe, Y.; Mabu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 A Title: A family of metabotropic glutamate receptors.
 A Reference number: JH0561; MUID:92110002; PMID:1305649
 A Molecule type: mRNA
 A Residues: 1-872 <TAN>
 A Cross-references: UNIPROT:P314421
 A Experimental source: brain
 C Comment: This protein is coupled to a G protein and evokes a variety of functions by II
 C Superfamily: metabotropic glutamate receptor 4
 C Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 P; 1-18/Domain: signal sequence #status predicted <SG>
 P; 19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

P; 568-590/Domain: transmembrane #status predicted <TRI>
 P; 637-655/Domain: transmembrane #status predicted <III>
 P; 680-700/Domain: transmembrane #status predicted <TIV>
 P; 726-742/Domain: transmembrane #status predicted <TRV>
 P; 761-782/Domain: transmembrane #status predicted <TVI>
 P; 795-819/Domain: transmembrane #status predicted <VII>
 P; 803, 286, 338, 402, 547/Binding site: phosphate (Ser) (covalent) #status predicted
 P; 601, 675, 827, 837, 843/Binding site: phosphate (Thr) (covalent) #status predicted
 P; 832/Binding site: phosphate (Ser) (covalent) #status predicted
 Query Match 15-61; Score 764; DB 2; Length 872;
 Best Local Similarity 25.3%; Pred. No. 8.1e-48;
 Matches 240; Conservative 169; Mismatches 402; Indels 136; Gaps 31;
 QY 18 LAFLWABIGSEKAEKEBEERTCRLGCKYDAENHS1VIGGIPIPDSTTPANESTLEPAS 77
 Db 10 LLLWGG-----AVAGPAKKVLTLEG-----DLVTLGGLEPVHQKGPAE----- 49
 QY 78 AKCEGFNFOR-PRMMKAMHMIKEINKRKDILPNITLGQIEDTCFRISKSYEAVALVPL- 135
 Db 50 --CGPYNEHHRG1QRLEARMLPALDRINRDPHLPGVRGAHILDSCSKTDTHALEQALDFVR 107
 QY 136 ---TGEBENR--PFRPNSTGA--FPAGIVGA-GGSP--LSVSPASRILGTYLQPVQSYTS 184
 Db 108 ASLSRGADGDSRHICPDCSYATSHSDAFTAVTGYIGGSYSDVSIQVANILRLRFOPIQSYAS 167
 QY 185 TCVLSDKYQFQPSYLRTIASDKIQSKAVVKKRQIQLQHGPWVWGAIAADDYDGKVGKTCPEK 244
 Db 168 TSARLSDSKRSRDFYARTVPPDPFQAKAMETILRPFWNTYVSTVASEDTGETGEAFLPE 227
 QY 245 MESANLICVATSETIPKVYSNEKMQKAVKA-VKTSTAKVIVLYTSDLSLSPLEMHHNI 303
 Db 228 APARNICVATSEKVGGRAMSRAFEGVYRALLQKPSARAVLFTRSEARELLAATQRLN- 286
 QY 304 TDTWLTBAW-ITSALLAKPFPYEGGTGATPAPSPVIPELKBFEDVHKNOPNDVVL 362
 Db 287 ASFTWASDGNAGALESTVAGSERAEGAITELAS--YPSDFASFYFQSOLDPNNSRNKPW 344
 QY 363 TIEFWQTAFAFNCTWPN-----SVPYNNVDRHVNMTGKEORLYDMSDQLCTGEKEKEDL 414
 Db 345 FPFPMWBRFHCSFRQRQDCAAHSLSRAVEPEQBSKIMFV----- 381
 QY 415 XNTYLDTSQSLRITKQCKOQVAYIAHGLDHLSR-CQ-----EGQGPFGNSNOQCAV1PTP 466
 Db 382 -----VNAVAAAHANHNMTRALCPNTTHLCDAWMPVNGRR----- 417
 QY 467 DFWQLMY-YMKRKF-----KSHEDEKWVILDDNGDILKNGHYDVLWHLDDGEBSFPTV 519
 Db 418 ---LYKDQVLNKFDAPPRAFDTDEVRFDRFGD-GIGRYNIFTYLRAGSGRYRQKV 471
 QY 520 GRFNFRTNPELIVIPTNSTIPNTES-RLPISVCTDVCPPSTGRGFVQREPTICCFDOSIP 578
 Db 472 GW-----ABGILDTSPIPWASPSGQPLPASRCSPCLQNEVKSV-QPGEVWCWLCIP 524
 QY 579 CADGHSVRSKPGERECBQGDEDWNAQSKSCTVKEYBLAYDAEGLPTLVLSVFGAFVV 638
 Db 525 COP--YEYRLDEFTCADGLGTYWPNASLTGCPBLQFVIRMGDAWAVGPVTLACLGALAT 582
 QY 639 LAVTAVYVIRHRTPLVNASDWGLFLIQVSLLIMLSSMLFDKPHANWSMAGQVTLALG 698
 Db 583 LFVTLGVYEVNRNATPVVVKASGRBLCYILGG3VPLCYCMTFVPTAKPSTAVCTLRRLGIGTA 642
 QY 699 FSLCSCLGKISSFLAYRISKSCTQIOLTS-KHPLTRKTVLISVLABIGCTAYLLEP 757
 Db 643 PSVYCYSALLTKTRNARIIFGARREGQPRPFTSPAQVAICLALGQOLLIVAAWVVEA 702
 QY 758 PMVYKOMESONTKII-LGCMNTSISBFLYMSMFGIDAPLALCFLTFWVAROLPDNTYEGKC 816
 Db 703 PRGKGETAPERREVTLRCNHRDASHMIGSL-AYNNVIALCTLYAFTTRKGCPENFNEAKF 761
 QY 817 TFGMLVFPFIIMMSFVYVPLSTKGFKFMAVEIPALLASSHG--LGGCIAPKCLILRP 874
 P; 19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

Db	762	IGFTMYTCIWIWALFLPITYVTSSDYRVQTTMCVSUSLGSVVLGCLFAPKLHILFQP	821	Qy	506	WHDDEGEISFVTVGFNFRSTNFELVPIPTNTTESSLPHSYCTDVCPPGTGRGF	565	
Qy	875	ERNTSEIVTCRVSITI-DNCIQLTSAFVSELENNTTIVSLDDRLV	919	Db	482	YQTNTTNPGYRLIGW--TDELQNI--EDMQGKGVRLPSYCTLPECKPGQ-RKK	534	
Db	822	QKN---VVSHRAPTSRGSSAAPRASANTCQGSQSQQFVTPVCNGREVV	865	Qy	566	VQREPICCFDSIPCAOGHVSKXPGECEQGEDYWSNAOKSCECVLKVEVEYLAYDBALGF	625	
RESULT 14				Db	535	TQKGTCWCWTEBPC-DGY-QYQFDENTCQHCPYDQPNENRTGGCONIPIKLEWHSPWAV	592	
A49874	metabotropic glutamate receptor 7 - rat	N; Alternative names: metabotropic glutamate receptor mGlur7		Qy	626	TIVLISVVEGAFLVNLAVTAVVYIHRHTPLVNVNSDWKQGLFQYLSLIMLSSMLFDIKPHN	685	
C; Species: Rattus norvegicus (Norway rat)				Db	593	IPIVFLAMGLIATIFMTRFYNDPPIVRAASGRELSYVLTGIFLCVIIITPMIAKEVDV	652	
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004				Qy	686	WSCMAGQVTLALGFSCLSLCLGKTSSEFLAYRI-SKSKTQLTSMMPLYRKIVLIVSILA	744	
C; Accession: A49874; 157954				Db	653	AVCSFPRVFLGIGMCISYAALLTKTTRI--YRIFEGKKSVTAPE-----LISPTS	701	
R; Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakaniishi, J. Biol. Chem. 269, 1231-1236, 1994				Qy	745	BIGCHAYLI-----LEPMV-----YKMGESONTKILIGCNBISIEFLYSM	786	
A; Title: Molecular characterization of a new metabotropic glutamate receptor mGlur7 couple				Db	702	QLA1-TSSLISLVQLLGPIFIWGVDPPNNIIDYDEHKTMNPBOARGVLKCDIDLQIICSL	760	
A; Reference number: A49874; MUID:94117433; PMID:8288585				Qy	787	FGIDAFIALICFLTRTFVAROLPDNYEGKCITFGMNVFFIIMSFPVYVLST-KGKEPKNA	845	
A; Status: preliminary; translated from GB/EMLB/DDBJ				Db	761	-GYSILLMMVTTCTVYAKTRGVOPENFAEKPIGFTMTTCIVLAFPLIFGFTAQSAAEKL	819	
A; Molecule type: mRNA				Qy	846	VB---IFAILAASSGHGCGIFPKCLLIIIRPERNTSE	880	
A; Residues: 1-15 <RES>				Db	820	IORTTLMISNSASYAVGMLYMPKYYIIIFPELNYQK	858	
R; Saugstad, J.A.; Kinzie, J.M.; Mulvihill, B.R.; Segerson, T.P.; Westbrook, G.L.				Db				
Nol. Pharmacol. 45, 371-372, 1994				RESULT 15				
A; Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid				A46742				
A; Reference number: 157954; MUID:9419260; PMID:8147123					metabotropic glutamate receptor, mGlur6 - rat			
A; Accession: 157954					C; Species: Rattus norvegicus (Norway rat)			
A; Status: preliminary; translated from GB/EMLB/DDBJ					C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004			
A; Molecule type: mRNA					C; Accession: A46742			
A; Residues: 1-915 <RE2>					R; Nakatima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakaniishi, J. Biol. Chem. 268, 11868-11873, 1993			
A; References: EMBL:U06832; PIDN:9459658					A; Cross-references: UNIPROT:P35349; GB:D13963; PIDN:9391856; PMID:8383366			
C; Genetics:					A; Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m			
A; Gene: mGlur7					A; Reference number: A46742; MUID:9328015; PMID:8383366			
C; Superfamily: metabotropic glutamate receptor 4					A; Accession: A46742			
C; Keywords: neurotransmitter receptor					A; Status: preliminary			
Query Match					A; Molecule type: nucleic acid			
Score 750; DB 2; Length 915;					A; Residues: 1-871 <NAK>			
Best Local Similarity 24.3%; Pred. No. 2.4e-47; Indels 120; Gaps 32;					A; Cross-references: UNIPROT:P35349; GB:D13963; PIDN:9391856; PMID:8383366			
Matches 214; Conservative 191; Mismatches 354; Score 750; DB 2; Length 915;					A; Experimental source: retina			
Db	49	VTLGGLPFPHAK-----GPSVPCCDIKRENGIHRLBEAMLYALDQINSDPNLLPN	99		C; Superfamily: metabotropic glutamate receptor 4			
Qy	53	LVIGGLPIDSRTIPANESILEPASA KACGEFNFOR-FRMVKAMHMIKEINKRDILPNI	111		C; Keywords: G protein-coupled receptor; transmembrane protein			
Db	112	TIGYQIFPDTCTISVETAVLVELTGQ--SEENPNEFRNSTGAFP-----AGIVGAGGS	162		Query Match			
Qy	100	TLGARILDTCSDRTYALEQSLTFLQVQI DTSVRCTINGEPFPVFKPEKVVGIGSGS	159		Best Local Similarity 24.9%; Pred. No. 6.4e-45; Gaps 28;			
Db	163	FLSVPAASRILGLLYLPQVGUTSTCVLISKYQPPSYLVRVIASDKIOSKAVVRIQHGW	222		Matches 217; Conservative 174; Mismatches 380; Indels 101;			
Qy	160	SVSI MYANLRLRFQIPOISI STASTAPELSDRRYDFFSRVPPSFQQA MDIVKA GWN	219		Qy	53	LVIGGLPIDSRTIPANESILEPASA KACGEF-NFQRPEWMKAMHMIKEINKRDILPNI	111
Db	223	WVGAIADDYDGKYGKTKFB-KMESANLCAVAFSETIPVSYNEKMRKAV-----KAV	274		Db	33	LTIGGLPFPHAR-----GA GRAGCAG ALKEQG YVHLAEMLYALDRVNADPELLPGY	83
Qy	226	DTPNSPAVIFTANDEDIKOIIAAKRA DQVGHFU----WVGSDSW-GKINPQPHQHSDIA	330		Qy	112	TIGYQIFPDTCTISVETAVLVELTGQENR-----PNFRNSTGAFPAGIV	157
Db	220	YVSTLASEGSYGEKG YESTFOISKEAGGCLIAQS VRIPO---ERKDRTIDFDRIKQL	275		Db	84	RUGARLUDTCSDRTYALEQSLTFLQVQI DTSVRCTINGEPFPVFKPEKVVGIGSGS	143
Qy	275	KTSTARVYLYTSDIDLSLFV-----LEMTHHNITDRTWIA TAWITSLAIIKPEPYFP	329		Qy	158	GAGGSFLSVPAASRILGLLYLPQVGUTSTCVLISKYQPPSYLVRVIASDKIOSKAVVRIQ	217
Db	276	DTPNSPAVIFTANDEDIKOIIAAKRA DQVGHFU----WVGSDSW-GKINPQPHQHSDIA	330		Db	144	GASASVSY SIMVANVLRIFAIPOLSYASAPLSDSTRYDFFSSVPPPSYQAQMVDIVR	203
Qy	330	GCTTGATP RPSVIPGKLF EFLYDVH PKNKD PNDVLTIEFWQTA WITSLAIIKPEPYFP	389		Qy	218	HFGWVWTGAIADDYDGKYGKTKFB-KMESANLCAVAFSETIPVSYNEKMRKAV-KAVK	275
Db	331	E GA ITIQPKRATVEG DDAYTSR TLENNENRNWFAEYNTEN FNC-----KLT	377		Db	204	ALGWNVYSTLASEGNGESVGEA FVQISREAGEVVIAQSIKLPREPKGEFH KVTRRLME	263
Qy	390	M TG---KEDRLYDMSDOLCTGEK LDKT YLDTSQLRATKQKQVAYA AHGELDHLSR	446		Qy	276	TSTPAKTVLYTSDIDLSLFV-----LVMENHNRHITDR-TWIA TAW---	331
Db	378	ISGSKKE D---TDRKCTGQERIKGD SN-YEQEGKVQTV-- IDAVYMAAHALHMKD	428		Db	264	TN ARGI IIFANEDDIRVLEATRQANLTGHFLWGSKSKISPILNLEEBAV--G	319
Qy	447	-CQE GQGPFGSNOCQAYI PTFDWKLYM KETIKF KSHEDKWL DKG HYDVLN 505						
Db	429	LCADYR3-----VCBEMEOAGGKLUK TIRHVNFNGSAGTPM FNKG DAP-GRYDIF Q	481					

QY 332 TIGPATRSVTPGLKGFELDYDHPNKDPNDVLTIWFOTAFNCTWPNSSVPYNDHRYNMT 391
 Db 320 AITLIPKRAISLDGFQFYTRSLLENRNTIWAEWEFENC-----KLSS 366
 QY 392 GKEDRLYDMSDQLCTGEKELEDLKNTYLTDSQLRITKQCKQAYTAIAIGLD - HLSRQE 449
 Db 367 GQGS ---DOSTRKCTGEERIGQ - DSAYEQBKGKVQFV - IDAVAYIAABALHSNHOALCP- 418
 QY 450 GQGPFGSNOOCAYIPTFDWQLMYYMBIKFKSHBBDKVNVLDDNGDLANGHYDVLNWLD 509
 QY 419 ----GHTGLCPANEPTDERTLLAHYIARFNGSAGTYYMENENGDAAPGRIDFOYCAT 472
 QY 510 DEGEIS - FVTVGFRNFIRSTNFELVITPTNSTIFWNTESRRLPHSVCTDVCPPGTGRGVQ 567
 Db 473 NGASSGGTOAVGON---AEALRIMDBVLRSQGDPHVPSQCSLPGPDBRKRNVK 526
 QY 568 REPICCFDSTPCADGHVSRKPGERECEQGEDYSNAQKSECYVKEVEYLAYDEBALGFTL 627
 Db 527 GVP-CCWHCERAC-DGY-RFQYDEFTECAACPGDMARPTPNTIGCRPTPVVRLTSSPWALP 583
 QY 628 VILSYVGAFAVLAIVAVYVTHRHPLVNAISDWQLGFLCIVSLLIMLSSMLP/DKPHNWS 687
 Db 584 LLLAVLGIMATTIMATFHNDTPIVASGREISVYLITGIPIAVATPLWAEPCMAI 643
 QY 688 CMAGCYTLAIGFSLCLSLCIGKTSSLPLAYRI ---SKSKTDTSMMPHLYRK1IVL-TSV 742
 Db 644 CAARLLLGIGTTLUSYSLTAKTRI ---YRIFEQKRVTPPPFIISTSQLVITFGRIS 700
 QY 743 LAEIGICLAYLILEPPMVYKNAMEQNT ---KILGNEISIEFLYMSMFGIDAFALL 796
 Db 701 LQVYGV-IAMLGAQPHASVTDYSECRVTDPEQARGVLC-DMSDSLIGCLGYSLLMMYT 758
 QY 797 CFLITTPVAROLPDNYEGRCITFGLVFFLIIWNSFVPTYLSTRGKPKNAVEIF----- 849
 Db 759 CTVYAIKARGVPETFNEAPIGFTMYTCIWIWAFVPIFFGTA --QSAAEKIYIQTTLT 815
 QY 850 -AIIASSHGLGCIAPKCLLILRPERNISE 880
 Db 816 VSLSIUSASVSLGMLTVPKVIVLHPETQVQK 847

Search completed: February 16, 2005, 16:37:58
 Job time : 42.2706 secs

THIS PAGE LEFT BLANK